

10/533277

1 / 18

JC17 Rec'd PCT/PTO 28 APR 2005

SEQUENCE LISTING

<110> National Institute of Agrobiological Sciences

<120> METHODS FOR DETERMINING GENETIC RESISTANCE OF PIGS TO DISEASES CAUSED
BY RNA VIRUSES

<130> MOA-A0214P

<140>

<141>

<150> JP 2002-313076

<151> 2002-10-28

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 2545

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (101).. (2092)

<220>

<221> polyA_signal

<222> (2517).. (2522)

<400> 1

gtaagtgtgg gagaacagcc ctgcatttct gctgacgggt caacgtcaca gcgtcaaaga 60

aaaggaaggt acatttcagc tgaactgac aaggaggaag atg gtt tat tcc agc 115

Met Val Tyr Ser Ser

1

5

tgt gaa agt aaa gaa cct gat tca gtt tct gca tcc aat cac ctg tta 163

Cys Glu Ser Lys Glu Pro Asp Ser Val Ser Ala Ser Asn His Leu Leu

10

15

20

cta aat ggg aat gat gaa ttg gtg gag aaa agt cac aaa aca ggg cct 211

Leu Asn Gly Asn Asp Glu Leu Val Glu Lys Ser His Lys Thr Gly Pro

25

30

35

gag aac aac ctg tac agc cag tac gag gag aaa gtg cgg ccc tgc atc 259

Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys Val Arg Pro Cys Ile

40

45

50

gac ctc atc gac tca ctg cgg gcc ctg ggc gtg gag cag gac ctg gcc 307

Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val Glu Gln Asp Leu Ala

55

60

65

ctg ccc gcc atc gcc gtc atc ggg gac cag agt tcg ggc aag agc tcc 355

Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser Ser Gly Lys Ser Ser

70

75

80

85

gtg ctg gag gcc ctg tcg ggg gtc gct ctc ccc aga ggc agc gga att 403

Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro Arg Gly Ser Gly Ile

90

95

100

gtg aca aga tgc cct ctt gtg ctg aaa ttg aaa aaa ctc gtg aac gaa 451

Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys Lys Leu Val Asn Glu

105

110

115

gaa gac gaa tgg aag ggc aaa gtc agt tac cgg gac agc gag att gag 499

Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg Asp Ser Glu Ile Glu

120

125

130

ctt tca gat gct tcg cag gtg gaa aag gaa gtc agc gca gcc cag att 547

Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val Ser Ala Ala Gln Ile

135

140

145

gcc atc gct ggg gaa ggc gtg gga atc agt cat gag cta atc agt ctg 595

Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His Glu Leu Ile Ser Leu

150

155

160

165

gag gtc agc tcc cct cat gtc cca gat ctg acc ctc ata gac ctt cct 643

Glu Val Ser Ser Pro His Val Pro Asp Leu Thr Leu Ile Asp Leu Pro

170

175

180

ggc atc acc agg gta gct gta ggc aat cag cca tac gac atc gaa tac 691

Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro Tyr Asp Ile Glu Tyr

185

190

195

cag atc aag tct ctg atc aag aag tac atc tgt aag cag gag acc atc 739

Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys Lys Gln Glu Thr Ile

200

205

210

aac ttg gtg gtg gtc ccc tgt aac gtg gac att gcc acc acg gag gcg 787

Asn Leu Val Val Val Pro Cys Asn Val Asp Ile Ala Thr Thr Glu Ala

215

220

225

ctg cgc atg gcc cag gag gtg gac ccc gaa gga gac agg acc atc ggg 835

Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly Asp Arg Thr Ile Gly

230

235

240

245

atc ttg acg aag ccg gat ctg gtg gac aaa ggc act gag gac aag ata 883

Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Ile

250

255

260

gtg gac gtg gcg aga aac ctg gtc ttc cac ctg aag aag ggc tac atg 931

Val Asp Val Ala Arg Asn Leu Val Phe His Leu Lys Lys Gly Tyr Met

265

270

275

att gtc aag tgc agg ggc cag cag gac atc cag gag cag ctg agc ctg 979

Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln Glu Gln Leu Ser Leu

280

285

290

gcc aag gcc ctg cag aag gag cag gcc ttc ttt gaa aac cac gca cat 1027

Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe Glu Asn His Ala His

295

300

305

ttc agg gat ctt ctg gag gaa ggg cgg gcc acg atc ccc tgc ctg gca 1075

Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr Ile Pro Cys Leu Ala

310

315

320

325

gaa aga ctg acc tct gaa ctc atc atg cac atc tgt aaa act ctg ccc 1123

Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile Cys Lys Thr Leu Pro

330

335

340

ctg tta gaa aac caa ata aaa gag agt cac cag aaa ata aca gag gag 1171

Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln Lys Ile Thr Glu Glu

345

350

355

tta cag aag tat ggc tcc gat att cca gag gat gaa agc ggg aag atg 1219

Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp Glu Ser Gly Lys Met

360

365

370

ttt ttt ctg ata gat aaa atc gat gca ttt aat agt gat atc act gct 1267

Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn Ser Asp Ile Thr Ala

375

380

385

ttg ata caa gga gag gaa ctg gtg gtg gag tac gag tgt cgg ctg ttt 1315

Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr Glu Cys Arg Leu Phe

390

395

400

405

acc aag atg cga aat gag ttc tgc aga tgg agt gct gtg gtt gaa aag 1363

Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser Ala Val Val Glu Lys

410

415

420

aat ttc aaa aat ggt tat gac gcc ata tgt aaa caa atc cag ctc ttc 1411

Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys Gln Ile Gln Leu Phe

425

430

435

gaa aat cag tac agg ggg aga gag ttg cca ggg ttt gtg aat tat aag 1459

Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly Phe Val Asn Tyr Lys

440

445

450

aca ttt gaa acc atc att aag aag cag gtc agt gtc ctg gaa gag cca 1507

Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser Val Leu Glu Glu Pro

455

460

465

gcc gtg gac atg ctg cac aca gtg act gat tta gtc cgg ctc gcc ttc 1555

Ala Val Asp Met Leu His Thr Val Thr Asp Leu Val Arg Leu Ala Phe
 470 475 480 485

aca gat gtt tca gaa aca aat ttt aat gaa ttt ttc aac ctc cac aga 1603
 Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe Phe Asn Leu His Arg
 490 495 500

act gcc aag tcc aaa att gaa gac att aaa tta gaa caa gaa aaa gaa 1651
 Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu Glu Gln Glu Lys Glu
 505 510 515

gct gag acg tcg atc cgg ctc cac ttc caa atg gag cag atc gtg tac 1699
 Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met Glu Gln Ile Val Tyr
 520 525 530

tgc cag gac cag gtc tat cgg ggc gcg ctg cag aag gtc aga gag aag 1747
 Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln Lys Val Arg Glu Lys
 535 540 545

gag gcg gaa gaa gaa aag aac aga aaa tca aac cag tac ttt ctg tcg 1795
 Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Asn Gln Tyr Phe Leu Ser
 550 555 560 565

tcg ccg gcc ccc tcc tca gac ccc tcc ata gcc gag atc ttt cag cac 1843
 Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala Glu Ile Phe Gln His
 570 575 580

ctg att gcc tac cat cag gag gtc ggc aag cgc atc tcc agc cac atc 1891

Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg Ile Ser Ser His Ile

585

590

595

cct ctg atc atc cag ttc ttc atc ctc cgg acc ttt ggg cag cag ctg 1939

Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr Phe Gly Gln Gln Leu

600

605

610

cag aag agc atg ctg cag ctg ctg cag aac aag gac caa tac gac tgg 1987

Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys Asp Gln Tyr Asp Trp

615

620

625

ctc ctg agg gag cgc agt gac acc agc gac aag agg aag ttc ctg aag 2035

Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys Arg Lys Phe Leu Lys

630

635

640

645

gag cgg ctg atg cgg ctg acc cag gct cgg cgc cgg ctc gcc aag ttc 2083

Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg Arg Leu Ala Lys Phe

650

655

660

cca ggc tga accggactct ccaggcggcc cggggtctcc agggcacgtc 2132

Pro Gly

tccaggcaac gaggaccaac ctccctccct aacagactag catcatgagc tcctgtttcg 2192

cacatcctcc tgtggtagt agactctaaa gccaccgtcc ctgctgtag tggctgagga 2252

cttagcaaga agctgtgata agcacgctgg ctgcaagcat caggccattt acttgaatga 2312

gccccgcaa cgcttcgcct cccgcgcctc tctccatccc tctctccatc cttctctcca 2372

tccctgtata ggatactggt ccccgcatag catcatagaa gggtcattct ggtttctgta 2432

caagcctttc acgcccattg tcttaggggc attacagcca cctgtgtgga tggatgcaca 2492

tagaagccta tttcttttat ttgtaataaa cttggttcta ccagcaaaaa aaa 2545

<210> 2

<211> 663

<212> PRT

<213> Sus scrofa

<400> 2

Met Val Tyr Ser Ser Cys Glu Ser Lys Glu Pro Asp Ser Val Ser Ala

1

5

10

15

Ser Asn His Leu Leu Leu Asn Gly Asn Asp Glu Leu Val Glu Lys Ser

20

25

30

His Lys Thr Gly Pro Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys

10 / 18

35

40

45

Val Arg Pro Cys Ile Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val

50

55

60

Glu Gln Asp Leu Ala Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser

65

70

75

80

Ser Gly Lys Ser Ser Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro

85

90

95

Arg Gly Ser Gly Ile Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys

100

105

110

Lys Leu Val Asn Glu Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg

115

120

125

Asp Ser Glu Ile Glu Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val

130

135

140

Ser Ala Ala Gln Ile Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His

145

150

155

160

Glu Leu Ile Ser Leu Glu Val Ser Ser Pro His Val Pro Asp Leu Thr

165

170

175

11 / 18

Leu Ile Asp Leu Pro Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro

180

185

190

Tyr Asp Ile Glu Tyr Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys

195

200

205

Lys Gln Glu Thr Ile Asn Leu Val Val Val Pro Cys Asn Val Asp Ile

210

215

220

Ala Thr Thr Glu Ala Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly

225

230

235

240

Asp Arg Thr Ile Gly Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly

245

250

255

Thr Glu Asp Lys Ile Val Asp Val Ala Arg Asn Leu Val Phe His Leu

260

265

270

Lys Lys Gly Tyr Met Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln

275

280

285

Glu Gln Leu Ser Leu Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe

290

295

300

Glu Asn His Ala His Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr

305

310

315

320

1 2 / 1 8

Ile Pro Cys Leu Ala Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile

325

330

335

Cys Lys Thr Leu Pro Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln

340

345

350

Lys Ile Thr Glu Glu Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp

355

360

365

Glu Ser Gly Lys Met Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn

370

375

380

Ser Asp Ile Thr Ala Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr

385

390

395

400

Glu Cys Arg Leu Phe Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser

405

410

415

Ala Val Val Glu Lys Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys

420

425

430

Gln Ile Gln Leu Phe Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly

435

440

445

Phe Val Asn Tyr Lys Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser

1 3 / 1 8

450

455

460

Val Leu Glu Glu Pro Ala Val Asp Met Leu His Thr Val Thr Asp Leu

465

470

475

480

Val Arg Leu Ala Phe Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe

485

490

495

Phe Asn Leu His Arg Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu

500

505

510

Glu Gln Glu Lys Glu Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met

515

520

525

Glu Gln Ile Val Tyr Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln

530

535

540

Lys Val Arg Glu Lys Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Asn

545

550

555

560

Gln Tyr Phe Leu Ser Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala

565

570

575

Glu Ile Phe Gln His Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg

580

585

590

1 4 / 1 8

Ile Ser Ser His Ile Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr

595

600

605

Phe Gly Gln Gln Leu Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys

610

615

620

Asp Gln Tyr Asp Trp Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys

625

630

635

640

Arg Lys Phe Leu Lys Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg

645

650

655

Arg Leu Ala Lys Phe Pro Gly

660

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 3

ctgaaagatc tcggctatgg agg

23

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 4

aagaagctga gacgtcgatc cggct

25

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 5

aagcgcattct ccagccacat c

21

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 6

aagacattgg gcgtgaaagg

20

<210> 7

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 7

ggggacaagt ttgtacaaaa aagcaggctg tcacagcgtc aaagaaaagg aag . 53

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 8

ggggaccact ttgtacaaga aagctgggtc cttctatgat gctatgcgg 49

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 9

18 / 18

agtgacagga gcgacaagag

20

<210> 10

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 10

cctggagagt ccggttca

18